

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/566,944
Source: IFWP
Date Processed by STIC: 02/14/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/566,944

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

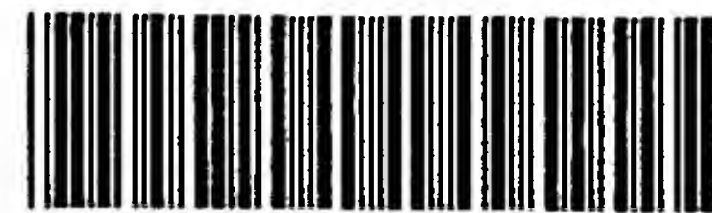
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 02/14/2006

PATENT APPLICATION: US/10/566,944

TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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3 <110> APPLICANT: Zank, Thorsten
4      Bauer, Jorg
5      Cirpus, Petra
6      Abbadi, Amine
7      Heinz, Ernst
8      Qiu, Xiao
9      Vrinten, Patricia
10     Sperling, Petra
11     Domergue, Frederic
12     Meyer, Astrid
13     Kirsch, Jelena
15 <120> TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY
ACIDS IN
16     TRANSGENIC ORGANISMS
18 <130> FILE REFERENCE: 12810-00193-US
C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/566,944
C--> 20 <141> CURRENT FILING DATE: 2006-02-01
20 <150> PRIOR APPLICATION NUMBER: DE 103 35 992.3
21 <151> PRIOR FILING DATE: 2003-08-01
23 <150> PRIOR APPLICATION NUMBER: DE 103 44 557.9
24 <151> PRIOR FILING DATE: 2003-09-24
26 <150> PRIOR APPLICATION NUMBER: DE 103 47 869.8
27 <151> PRIOR FILING DATE: 2003-10-10
29 <150> PRIOR APPLICATION NUMBER: DE 103 59 593.7
30 <151> PRIOR FILING DATE: 2003-12-18
32 <150> PRIOR APPLICATION NUMBER: DE 10 2004 009 457.8
33 <151> PRIOR FILING DATE: 2004-02-27
35 <150> PRIOR APPLICATION NUMBER: DE 10 2004 012 370.5
36 <151> PRIOR FILING DATE: 2004-03-13
38 <150> PRIOR APPLICATION NUMBER: DE 10 2004 024 014.0
39 <151> PRIOR FILING DATE: 2004-05-14
41 <160> NUMBER OF SEQ ID NOS: 192
43 <170> SOFTWARE: PatentIn version 3.1
46 <210> SEQ ID NO: 1
47 <211> LENGTH: 1266
48 <212> TYPE: DNA
49 <213> ORGANISM: Euglena gracilis
51 <220> FEATURE:
52 <221> NAME/KEY: CDS
53 <222> LOCATION: (1)..(1266)
54 <223> OTHER INFORMATION: delta8-desaturase
56 <400> SEQUENCE: 1
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58 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr

```

48

RAW SEQUENCE LISTING

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TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

59	1			5				10				15					
61	tat	gat	gtg	tct	gcc	tgg	gtc	aat	ttc	cac	cct	ggt	ggt	gcg	gaa	att	96
62	Tyr	Asp	Val	Ser	Ala	Trp	Val	Asn	Phe	His	Pro	Gly	Gly	Ala	Glu	Ile	
63				20				25				30					
65	ata	gag	aat	tac	caa	gga	agg	gat	gcc	act	gat	gcc	ttc	atg	gtt	atg	144
66	Ile	Glu	Asn	Tyr	Gln	Gly	Arg	Asp	Ala	Thr	Asp	Ala	Phe	Met	Val	Met	
68			35					40				45					
70	cac	tct	caa	gaa	gcc	ttc	gac	aag	ctc	aag	cgc	atg	ccc	aaa	atc	aat	192
71	His	Ser	Gln	Glu	Ala	Phe	Asp	Lys	Leu	Lys	Arg	Met	Pro	Lys	Ile	Asn	
72		50						55				60					
74	ccc	agt	tct	gag	ttg	cca	ccc	cag	gct	gca	gtg	aat	gaa	gct	caa	gag	240
75	Pro	Ser	Ser	Glu	Leu	Pro	Pro	Gln	Ala	Ala	Val	Asn	Glu	Ala	Gln	Glu	
76	65					70				75					80		
78	gat	ttc	cgg	aag	ctc	cga	gaa	gag	ttg	atc	gca	act	ggc	atg	ttt	gat	288
79	Asp	Phe	Arg	Lys	Leu	Arg	Glu	Glu	Leu	Ile	Ala	Thr	Gly	Met	Phe	Asp	
80				85				90				95					
82	gcc	tcc	ccc	ctc	tgg	tac	tca	tac	aaa	atc	agc	acc	aca	ctg	ggc	ctt	336
83	Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu	
84			100					105				110					
86	gga	gtg	ctg	ggt	tat	ttc	ctg	atg	gtt	cag	tat	cag	atg	tat	ttc	att	384
87	Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile	
88		115				120			125								
90	ggg	gca	gtg	ttg	ctt	ggg	atg	cac	tat	caa	cag	atg	ggc	tgg	ctt	tct	432
91	Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser	
92		130				135			140								
94	cat	gac	att	tgc	cac	cac	cag	act	ttc	aag	aac	cgg	aac	tgg	aac	aac	480
95	His	Asp	Ile	Cys	His	His	Gln	Thr	Phe	Lys	Asn	Arg	Asn	Trp	Asn	Asn	
96	145			150				155				160					
98	ctc	gtg	gga	ctg	gta	ttt	ggc	aat	ggt	ctg	caa	ggt	ttt	tcc	gtg	aca	528
99	Leu	Val	Gly	Leu	Val	Phe	Gly	Asn	Gly	Leu	Gln	Gly	Phe	Ser	Val	Thr	
101			165					170				175					
103	tgc	tgg	aag	gac	aga	cac	aat	gca	cat	cat	tcg	gca	acc	aat	gtt	caa	576
104	Cys	Trp	Lys	Asp	Arg	His	Asn	Ala	His	His	Ser	Ala	Thr	Asn	Val	Gln	
105			180					185				190					
107	ggg	cac	gac	cct	gat	att	gac	aac	ctc	ccc	ctc	tta	gcc	tgg	tct	gag	624
108	Gly	His	Asp	Pro	Asp	Ile	Asp	Asn	Leu	Pro	Leu	Leu	Ala	Trp	Ser	Glu	
109		195				200			205								
111	gat	gac	gtc	aca	cgg	gcg	tca	ccg	att	tcc	cgc	aag	ctc	att	cag	ttc	672
112	Asp	Asp	Val	Thr	Arg	Ala	Ser	Pro	Ile	Ser	Arg	Lys	Leu	Ile	Gln	Phe	
113		210				215			220								
115	cag	cag	tat	tat	ttc	ttg	gtc	atc	tgt	atc	ttg	ttg	cgg	ttc	att	tgg	720
116	Gln	Gln	Tyr	Tyr	Phe	Leu	Val	Ile	Cys	Ile	Leu	Leu	Arg	Phe	Ile	Trp	
117	225				230			235				240					
119	tgt	ttc	cag	agc	gtg	ttg	acc	gtg	cgc	agt	ctg	aag	gac	aga	gat	aac	768
120	Cys	Phe	Gln	Ser	Val	Leu	Thr	Val	Arg	Ser	Leu	Lys	Asp	Arg	Asp	Asn	
121			245					250				255					
123	caa	ttc	tat	cgc	tct	cag	tat	aag	aag	gag	gcc	att	ggc	ctc	gcc	ctg	816
124	Gln	Phe	Tyr	Arg	Ser	Gln	Tyr	Lys	Lys	Glu	Ala	Ile	Gly	Leu	Ala	Leu	
125			260					265				270					

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/566,944

DATE: 02/14/2006

TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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127 cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc      864
128 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
129      275      280      285
131 ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc      912
132 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
135      290      295      300
137 ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc      960
138 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
139 305      310      315      320
141 ggg gac tcg gtc ttg gat ggc cat gga ttc tcg gtt ggc cag atc cat      1008
142 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
143      325      330      335
145 gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga      1056
146 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
147      340      345      350
149 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc      1104
150 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
151      355      360      365
153 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag      1152
154 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
155      370      375      380
157 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc      1200
158 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
159 385      390      395      400
161 ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc      1248
162 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
163      405      410      415
165 gcg ggg aag gct cta taa      1266
166 Ala Gly Lys Ala Leu
168      420
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 421
173 <212> TYPE: PRT
174 <213> ORGANISM: Euglena gracilis
176 <400> SEQUENCE: 2
178 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
179 1      5      10      15
182 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
183      20      25      30
186 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
187      35      40      45
190 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
191      50      55      60
194 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
195 65      70      75      80
198 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
199      85      90      95
202 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
203      100      105      110

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RAW SEQUENCE LISTING

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DATE: 02/14/2006

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Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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206 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
207      115      120      125
210 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
211      130      135      140
214 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
215 145      150      155      160
218 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
219      165      170      175
222 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
223      180      185      190
226 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
227      195      200      205
230 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
231      210      215      220
234 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
235 225      230      235      240
238 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
239      245      250      255
242 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
243      260      265      270
246 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
247      275      280      285
250 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
251      290      295      300
254 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
255 305      310      315      320
258 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
259      325      330      335
262 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
263      340      345      350
266 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
267      355      360      365
270 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
271      370      375      380
274 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
275 385      390      395      400
278 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
279      405      410      415
282 Ala Gly Lys Ala Leu
283      420
286 <210> SEQ ID NO: 3
287 <211> LENGTH: 777
288 <212> TYPE: DNA
289 <213> ORGANISM: Isochrysis galbana
291 <220> FEATURE:
292 <221> NAME/KEY: CDS
293 <222> LOCATION: (1)..(777)
294 <223> OTHER INFORMATION: delta9-elongase
296 <400> SEQUENCE: 3

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RAW SEQUENCE LISTING

DATE: 02/14/2006

PATENT APPLICATION: US/10/566,944

TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

297	atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc	48
298	Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr	
299	1 5 10 15	
301	gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg	96
302	Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro	
303	20 25 30	
305	ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg	144
306	Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg	
307	35 40 45	
309	acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg	192
310	Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu	
311	50 55 60	
313	agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc	240
314	Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly	
315	65 70 75 80	
317	gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag	288
318	Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln	
319	85 90 95	
321	tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag	336
322	Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys	
323	100 105 110	
325	gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg	384
326	Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu	
327	115 120 125	
329	agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat	432
330	Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp	
331	130 135 140	
333	gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg	480
334	Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met	
335	145 150 155 160	
337	ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc	528
338	Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu	
339	165 170 175	
341	acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg	576
342	Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met	
343	180 185 190	
345	cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc	624
346	Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile	
347	195 200 205	
349	aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct	672
350	Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala	
351	210 215 220	
353	ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt	720
354	Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe	
355	225 230 235 240	
357	ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag	768
358	Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys	
359	245 250 255	
361	cag ctc tag	777

<210> SEQ ID NO 115
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Unknown

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(13)

<223> OTHER INFORMATION: Xaa in the sequence at position 2, 3, 4, 6, 7, 8 and 9
has the meaning given in Table A.

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(13)

<223> OTHER INFORMATION: Consensus

<400> SEQUENCE: 115

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa
1 5 10

Invalid Response. Xaa¹ Represents
Single Amino Acid. P/s see Item
#9 in Error
Summary Sheet.

Tyr at this
Location

F41

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/566,944

DATE: 02/14/2006
TIME: 12:55:18

Input Set : F:\Sequence listing (12810-00193-US).txt
Output Set: N:\CRF4\02142006\J566944.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:115; Xaa Pos. 2,3,4,6,7,10,13
Seq#:116; Xaa Pos. 3,4,5,6
Seq#:139; Xaa Pos. 3,4
Seq#:140; Xaa Pos. 2,3,5,6
Seq#:141; Xaa Pos. 3
Seq#:142; Xaa Pos. 5,6
Seq#:185; N Pos. 3,18
Seq#:186; N Pos. 3,9,12,15,21

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:115; Line(s) 12392
Seq#:116; Line(s) 12415
Seq#:140; Line(s) 13593
Seq#:142; Line(s) 13635

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/566,944

DATE: 02/14/2006

TIME: 12:55:18

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0
L:12426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0
L:13581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:13602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:13623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:13646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:14407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185 after pos.:0
L:14426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:186 after pos.:0